

RAW SEQUENCE LISTING

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Application Serial Number: 10/781,659
Source: JFLOO
Date Processed by STIC: 07/26/2005

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RAW SEQUENCE LISTING

DATE: 07/26/2005

PATENT APPLICATION: US/10/781,659

TIME: 09:31:21

Input Set : N:\Crif3\RULE60\10781659.raw

Output Set: N:\CRF4\07262005\J781659.raw

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1 <110> APPLICANT: ITOH, Kyogo et al.
2 <120> TITLE OF INVENTION: NOVEL TUMOR ANTIGEN PROTEIN SART-3 AND TUMOR ANTIGEN
3   PEPTIDES THEREOF
4 <130> FILE REFERENCE: 0020-4817P
5 <140> CURRENT APPLICATION NUMBER: US/10/781,659
6 <141> CURRENT FILING DATE: 2004-02-20
7 <150> PRIOR APPLICATION NUMBER: US/09/763,985
8 <151> PRIOR FILING DATE: 2001-02-28
9 <160> NUMBER OF SEQ ID NOS: 64
10 <170> SOFTWARE: PatentIn version 3.1
12 <210> SEQ ID NO: 1
13 <211> LENGTH: 3798
14 <212> TYPE: DNA
15 <213> ORGANISM: Homo sapiens
16 <220> FEATURE:
17 <221> NAME/KEY: CDS
18 <222> LOCATION: (12)..(2900)
19 <223> OTHER INFORMATION:
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21   ccacgcgtcc g atg gcg act gcg gcc gaa acc tcg gct tca gaa ccc gag      50
22           Met Ala Thr Ala Ala Glu Thr Ser Ala Ser Glu Pro Glu
23           1               5               10
24   gct gag tcc aag gct ggg ccc aag gct gac gga gag gag gat gag gtt      98
25   Ala Glu Ser Lys Ala Gly Pro Lys Ala Asp Gly Glu Glu Asp Glu Val
26           15               20               25
27   aag gcg gct agg aca agg aga aag gtg tta tcg cgg gct gtg gcc gct      146
28   Lys Ala Ala Arg Thr Arg Arg Lys Val Leu Ser Arg Ala Val Ala Ala
29           30               35               40               45
30   gcg aca tac aag acc atg ggg cca gcg tgg gat cag cag gag gaa ggc      194
31   Ala Thr Tyr Lys Thr Met Gly Pro Ala Trp Asp Gln Gln Glu Glu Gly
32           50               55               60
33   gtg agc gag agc gat ggg gat gag tac gcc atg gct tcc tcc gcg gag      242
34   Val Ser Glu Ser Asp Gly Asp Glu Tyr Ala Met Ala Ser Ser Ala Glu
35           65               70               75
36   agc tcc ccc ggg gag tac gag tgg gaa tat gac gaa gag gag gag aaa      290
37   Ser Ser Pro Gly Glu Tyr Glu Trp Glu Tyr Asp Glu Glu Glu Lys
38           80               85               90
39   aac cag ctg gag att gag aga ctg gag gag cag ttg tct atc aac gtc      338
40   Asn Gln Leu Glu Ile Glu Arg Leu Glu Glu Gln Leu Ser Ile Asn Val
41           95               100              105
42   tat gac tac aac tgc cat gtg gac ttg atc aga ctg ctc agg ctg gaa      386
43   Tyr Asp Tyr Asn Cys His Val Asp Leu Ile Arg Leu Leu Arg Leu Glu
44           110              115              120              125

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45	ggg gag ctt acc aag gtg agg atg gcc cgc cag aag atg agt gaa atc	434
46	Gly Glu Leu Thr Lys Val Arg Met Ala Arg Gln Lys Met Ser Glu Ile	
47	130 135 140	
48	ttt ccc ttg act gaa gag ctc tgg ctg gag tgg ctg cat gac gag atc	482
49	Phe Pro Leu Thr Glu Glu Leu Trp Leu Glu Trp Leu His Asp Glu Ile	
50	145 150 155	
51	agc atg gcc cag gat ggc ctg gac aga gag cac gtg tat gac ctc ttt	530
52	Ser Met Ala Gln Asp Gly Leu Asp Arg Glu His Val Tyr Asp Leu Phe	
53	160 165 170	
54	gag aaa gcc gtg aag gat tac att tgt cct aac att tgg cta gag tat	578
55	Glu Lys Ala Val Lys Asp Tyr Ile Cys Pro Asn Ile Trp Leu Glu Tyr	
56	175 180 185	
57	ggc cag tac tca gtt ggt ggg att ggt cag aaa ggt ggc ctt gag aaa	626
58	Gly Gln Tyr Ser Val Gly Gly Ile Gly Gln Lys Gly Gly Leu Glu Lys	
59	190 195 200 205	
60	gtt cgc tcc gtg ttt gaa agg gct ctc tgc tct gtt ggt tta cat atg	674
61	Val Arg Ser Val Phe Glu Arg Ala Leu Ser Ser Val Gly Leu His Met	
62	210 215 220	
63	acc aaa gga ctc gcc ctc tgg gag gct tac cga gag ttt gaa agt gcg	722
64	Thr Lys Gly Leu Ala Leu Trp Glu Ala Tyr Arg Glu Phe Glu Ser Ala	
65	225 230 235	
66	att gtg gaa gct gct cgg ctt gag aaa gtc cac agt ctt ttc cgg cga	770
67	Ile Val Glu Ala Ala Arg Leu Glu Lys Val His Ser Leu Phe Arg Arg	
68	240 245 250	
69	cag ttg gcg atc cca ctc tat gat atg gag gcc aca ttt gca gag tat	818
70	Gln Leu Ala Ile Pro Leu Tyr Asp Met Glu Ala Thr Phe Ala Glu Tyr	
71	255 260 265	
72	gaa gaa tgg tca gaa gac cca ata cca gag tca gta att cag aac tat	866
73	Glu Glu Trp Ser Glu Asp Pro Ile Pro Glu Ser Val Ile Gln Asn Tyr	
74	270 275 280 285	
75	aac aaa gca cta cag cag ctg gag aaa tat aaa ccc tat gaa gaa gca	914
76	Asn Lys Ala Leu Gln Gln Leu Glu Lys Tyr Lys Pro Tyr Glu Glu Ala	
77	290 295 300	
78	ctg ttg cag gca gag gca cca agg ctg gca gaa tat caa gca tat atc	962
79	Leu Leu Gln Ala Glu Ala Pro Arg Leu Ala Glu Tyr Gln Ala Tyr Ile	
80	305 310 315	
81	gat ttt gag atg aaa att ggc gat cct gct cgc att cag ttg atc ttt	1010
82	Asp Phe Glu Met Lys Ile Gly Asp Pro Ala Arg Ile Gln Leu Ile Phe	
83	320 325 330	
84	gag cgc gcc ctg gtc gag aac tgc ctt gtc cca gac tta tgg atc cgt	1058
85	Glu Arg Ala Leu Val Glu Asn Cys Leu Val Pro Asp Leu Trp Ile Arg	
86	335 340 345	
87	tac agt cag tac cta gat cga caa ctg aaa gta aag gat ttg gtt tta	1106
88	Tyr Ser Gln Tyr Leu Asp Arg Gln Leu Lys Val Lys Asp Leu Val Leu	
89	350 355 360 365	
90	tct gta cat aac cgc gct att aga aac tgc ccc tgg aca gtt gcc tta	1154
91	Ser Val His Asn Arg Ala Ile Arg Asn Cys Pro Trp Thr Val Ala Leu	
92	370 375 380	
93	tgg agt cgg tac ctc ttg gcc atg gag aga cat gga gtt gat cat caa	1202

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Input Set : N:\Crif3\RULE60\10781659.raw

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94	Trp Ser Arg Tyr Leu Leu Ala Met Glu Arg His Gly Val Asp His Gln	
95	385 390 395	
96	gta att tct gta acc ttc gag aaa gct ttg aat gcc ggc ttc atc cag	1250
97	Val Ile Ser Val Thr Phe Glu Lys Ala Leu Asn Ala Gly Phe Ile Gln	
98	400 405 410	
99	gcc act gat tat gtg gag att tgg cag gca tac ctt gat tac ctg agg	1298
100	Ala Thr Asp Tyr Val Glu Ile Trp Gln Ala Tyr Leu Asp Tyr Leu Arg	
101	415 420 425	
102	aga agg gtt gat ttc aaa caa gac tcc agt aaa gag ctg gag gag ttg	1346
103	Arg Arg Val Asp Phe Lys Gln Asp Ser Ser Lys Glu Leu Glu Glu Leu	
104	430 435 440 445	
105	agg gcc gcc ttt act cgt gcc ttg gag tat ctg aag cag gag gtg gaa	1394
106	Arg Ala Ala Phe Thr Arg Ala Leu Glu Tyr Leu Lys Gln Glu Val Glu	
107	450 455 460	
108	gag cgt ttc aat gag agt ggt gat cca agc tgc gtg att atg cag aac	1442
109	Glu Arg Phe Asn Glu Ser Gly Asp Pro Ser Cys Val Ile Met Gln Asn	
110	465 470 475	
111	tgg gct agg att gag gct cga ctg tgc aat aac atg cag aaa gct cgg	1490
112	Trp Ala Arg Ile Glu Ala Arg Leu Cys Asn Asn Met Gln Lys Ala Arg	
113	480 485 490	
114	gaa ctc tgg gat agc atc atg acc aga gga aat gcc aag tac gcc aac	1538
115	Glu Leu Trp Asp Ser Ile Met Thr Arg Gly Asn Ala Lys Tyr Ala Asn	
116	495 500 505	
117	atg tgg cta gag tat tac aac ctg gaa aga gct cat ggt gac acc cag	1586
118	Met Trp Leu Glu Tyr Tyr Asn Leu Glu Arg Ala His Gly Asp Thr Gln	
119	510 515 520 525	
120	cac tgc cgg aag gct ctg cac cgg gcc gtc cag tgc acc agt gac tac	1634
121	His Cys Arg Lys Ala Leu His Arg Ala Val Gln Cys Thr Ser Asp Tyr	
122	530 535 540	
123	cca gag cac gtc tgc gaa gtg tta ctc acc atg gag agg aca gaa ggt	1682
124	Pro Glu His Val Cys Glu Val Leu Leu Thr Met Glu Arg Thr Glu Gly	
125	545 550 555	
126	tct tta gaa gat tgg gat ata gct gtt cag aaa act gaa acc cga tta	1730
127	Ser Leu Glu Asp Trp Asp Ile Ala Val Gln Lys Thr Glu Thr Arg Leu	
128	560 565 570	
129	gct cgt gtc aat gag cag aga atg aag gct gca gag aag gaa gca gcc	1778
130	Ala Arg Val Asn Glu Gln Arg Met Lys Ala Ala Glu Lys Glu Ala Ala	
131	575 580 585	
132	ctt gtg cag caa gaa gaa gaa aag gct gaa caa cgg aaa aga gct cgg	1826
133	Leu Val Gln Gln Glu Glu Glu Lys Ala Glu Gln Arg Lys Arg Ala Arg	
134	590 595 600 605	
135	gct gag aag aaa gcg tta aaa aag aag aaa aag atc aga ggc cca gag	1874
136	Ala Glu Lys Lys Ala Leu Lys Lys Lys Lys Lys Ile Arg Gly Pro Glu	
137	610 615 620	
138	aag cgc gga gca gat gag gac gat gag aaa gag tgg ggc gat gat gaa	1922
139	Lys Arg Gly Ala Asp Glu Asp Asp Glu Lys Glu Trp Gly Asp Asp Glu	
140	625 630 635	
141	gaa gag cag cct tcc aaa cgc aga agg gtc gag aac agc atc cct gca	1970
142	Glu Glu Gln Pro Ser Lys Arg Arg Arg Val Glu Asn Ser Ile Pro Ala	

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192   agg acg cag ctg tct cta ctg cct cgt gcc ctg cag cgc cca agt gct      2786
193   Arg Thr Gln Leu Ser Leu Leu Pro Arg Ala Leu Gln Arg Pro Ser Ala
194   910                               915                               920                               925
195   gca gct cct cag gct gag aac ggc cct gcc gcg gct cct gca gtt gcc      2834
196   Ala Ala Pro Gln Ala Glu Asn Gly Pro Ala Ala Ala Pro Ala Val Ala
197                               930                               935                               940
198   gcc cca gca gcc acc gag gca ccc aag atg tcc aat gcc gat ttt gcc      2882
199   Ala Pro Ala Ala Thr Glu Ala Pro Lys Met Ser Asn Ala Asp Phe Ala
200                               945                               950                               955
201   aag ctg ttt ctg aga aag tgaacgggac gctgggagac aggaaatgcc      2930
202   Lys Leu Phe Leu Arg Lys
203   960
204   ttacttcact ctggcccggc ggacctccca ccaccagca gtgcactggg gatggacagg      2990
205   cctgggtgtgc tgcgtgctcg caaccacaga tggctcctcg gctttagaca gaaaggggaa      3050
206   ggggttctaa gtcaagagcc tttcagtgtc ccctcatatt gagggcagtg gcagaaaagt      3110
207   gaccactctg caggctgggc ccaggatgtg gtgtcctgag atagttttgt atcttaaaga      3170
208   ctgaggcaca gaagcgaaac gagaacacac tgtttttgag acacagttgt ccaaagtgtt      3230
209   ctggccagct ccggcccctt tttgtatgac acttctcttc caccctgcac agcacatgtg      3290
210   cccgtcattc ttttaatttt aaaagatgaa atggcagatg ctagtaattc acagaatggc      3350
211   ctcttggtggg ggtgggtctg aggggaagtca gctataaaac atttgctgga gttttgttca      3410
212   atggggctgt gcatttttat attatgtgtt tgtaaataac atgtcagccc ttgtttcatg      3470
213   tttcctaaaa gcagaatatt tgcaacattt gttttgtata ggaattattt gtgccacctg      3530
214   ctgtggactg ttttctttgc ctagtgacta gtgacctgtg ttgtctaaac atgagtttca      3590
215   gcccttttgt tttgtttaat accatgtcaa atgcaaaact caattctccc catttagctt      3650
216   tattaactg acgttctctt caaaacttct tgctgaatgg tactcagatg tgcattcaca      3710
217   tacagatgtg ttttgaagtg ggtgtacctt gctttaccta atagatgtgt aaatagaact      3770
218   tttgtaagtc aaaaaaaaaa aaaaaaaaaa      3798
220 <210> SEQ ID NO: 2
221 <211> LENGTH: 963
222 <212> TYPE: PRT
223 <213> ORGANISM: Homo sapiens
224 <400> SEQUENCE: 2
225   Met Ala Thr Ala Ala Glu Thr Ser Ala Ser Glu Pro Glu Ala Glu Ser
226   1                               5                               10                               15
227   Lys Ala Gly Pro Lys Ala Asp Gly Glu Glu Asp Glu Val Lys Ala Ala
228   20                               25                               30
229   Arg Thr Arg Arg Lys Val Leu Ser Arg Ala Val Ala Ala Thr Tyr
230   35                               40                               45
231   Lys Thr Met Gly Pro Ala Trp Asp Gln Gln Glu Glu Gly Val Ser Glu
232   50                               55                               60
233   Ser Asp Gly Asp Glu Tyr Ala Met Ala Ser Ser Ala Glu Ser Ser Pro
234   65                               70                               75                               80
235   Gly Glu Tyr Glu Trp Glu Tyr Asp Glu Glu Glu Glu Lys Asn Gln Leu
236   85                               90                               95
237   Glu Ile Glu Arg Leu Glu Glu Gln Leu Ser Ile Asn Val Tyr Asp Tyr
238   100                              105                              110
239   Asn Cys His Val Asp Leu Ile Arg Leu Leu Arg Leu Glu Gly Glu Leu
240   115                              120                              125
241   Thr Lys Val Arg Met Ala Arg Gln Lys Met Ser Glu Ile Phe Pro Leu

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:53; Xaa Pos. 2,10
Seq#:54; Xaa Pos. 2,10
Seq#:55; Xaa Pos. 2,9
Seq#:56; Xaa Pos. 2,9
Seq#:57; Xaa Pos. 2,10
Seq#:58; Xaa Pos. 2,9
Seq#:59; Xaa Pos. 2,9
Seq#:60; Xaa Pos. 2,9
Seq#:61; Xaa Pos. 2,9
Seq#:62; Xaa Pos. 2,9
Seq#:63; Xaa Pos. 2,9
Seq#:64; Xaa Pos. 2,9

VERIFICATION SUMMARY

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Input Set : N:\Cr3\RULE60\10781659.raw

Output Set: N:\CRF4\07262005\J781659.raw

L:20 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:0
L:753 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:756 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:53
L:759 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:53
L:760 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53 after pos.:0
L:769 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:772 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:54
L:775 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:54
L:776 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54 after pos.:0
L:785 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:788 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:55
L:791 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:55
L:792 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55 after pos.:0
L:801 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:804 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:56
L:807 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:56
L:808 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56 after pos.:0
L:817 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:820 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:57
L:823 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:57
L:824 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:0
L:833 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:836 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:58
L:839 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:58
L:840 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:0
L:849 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:852 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:59
L:855 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:59
L:856 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59 after pos.:0
L:865 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:868 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:60
L:871 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:60
L:872 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60 after pos.:0
L:881 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:884 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:61
L:887 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:61
L:888 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61 after pos.:0
L:897 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:900 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:62
L:903 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:62
L:904 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62 after pos.:0
L:913 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:916 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:63
L:919 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:63
L:920 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63 after pos.:0
L:929 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:932 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:64
L:935 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:64

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L:936 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64 after pos.:0